

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 3, 2005, 13:50:51 ; Search time 170 Seconds
(without alignments)

Perfect score: US-10-018-964-3_COPY_1_15
Sequence: 1 YSGPPSGARRRNCYE 15

Title: US-10-018-964-3_COPY_1_15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03;*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	
1	87	100.0	319	1 MYOD_HUMAN	P15172 homo sapien	
2	87	100.0	320	2 O75321	O75321 homo sapien	
3	84	96.6	150	2 O77799	O77799 bov tauris	
4	84	96.6	318	2 Q7Y822	Q7Y822 bos tauris	
5	84	96.6	319	1 MYOD_PIG	P49811 sus scrofa	
6	84	96.5	319	1 MYOD_SHEEP	P29331 ovis aries	
7	77	63	72.4	318	1 MYOD_MOUSE	P10085 mus musculus
8	8	63	72.4	318	1 MYOD_RAT	Q02346 rattus norvegicus
9	63	72.4	318	2 Q8CB11	Q8CB11 mus musculus	
10	60	69.0	297	2 P21572	P21572 equus caballus	
11	60	69.0	297	2 O6DV59	O6DV59 equus caballus	
12	60	69.0	298	1 MYOD_CHICK	P16079 gallus gallus	
13	57	65.5	289	1 P13904	P13904 xenopus laevis	
14	57	65.5	289	2 Q8AVZ0	Q8AVZ0 xenopus laevis	
15	50	57.5	172	2 Q7SV41	Q7SV41 physcomitrella patens	
16	50	57.5	417	2 Q7SV42	Q7SV42 physcomitrella patens	
17	49.5	56.9	288	2 P07T09	P07T09 xenopus tropicalis	
18	48	55.2	652	2 Q8BSW9	Q8BSW9 xenopus tropicalis	
19	48	55.2	652	2 Q8W8X0	Q8W8X0 xenopus tropicalis	
20	47	54.0	271	1 P15407	P15407 homo sapien	
21	47	54.0	273	1 P15407	P15407 homo sapien	
22	47	54.0	273	2 Q7TMU4	Q7TMU4 mus musculus	
23	47	54.0	275	1 P10158	P10158 ratmus norvegicus	
24	47	54.0	652	2 Q8BSW1	Q8BSW1 dugesia tigridia	
25	47	54.0	2340	2 Q7RDO1	Q7RDO1 plasmodium falciparum	
26	46	52.9	932	2 Q9P966	Q9P966 eimeria tenella	
27	45.5	52.3	313	2 Q7RE93	Q7RE93 oryza sativa	
28	45	51.7	120	2 Q9WV15	Q9WV15 bacteriophaga	
29	45	51.7	139	2 Q6ZAR3	Q6ZAR3 oryza sativa	
30	45	51.7	1184	1 D83978	D83978 mycobacterium tuberculosis	
31	45	51.7	1184	1 DP3A_MYC0	DP3A_MYC0	

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CC
 DR EMBL; X56771; CAA40000.1; -.
 DR EMBL; X17850; CAA35640.1; -.
 DR PIR; S26827; S26827.
 DR HSSP; P1085; IMDY.
 DR TRANSFAC; T00519; -.
 DR Genew; HGNC; 7611; MNOD1.
 DR MIM; 159701; -.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:003705; P:RNA polymerase II transcription coactivator activity; TAS.
 DR GO; GO:003713; P:transcription coactivator activity; TAS.
 DR GO; GO:0017519; P:myogenesisB; TAS.
 DR GO; GO:005468; P:protein amino acid phosphorylation; TAS.
 DR GO; GO:006357; P:regulation of transcription from Pol II promoter; TAS.
 DR InterPro; IPR002546; Basic.
 DR InterPro; IPR001092; HLH_basic.
 DR PFAM; PF01586; Basic; 1.
 DR Pfam; PF00010; HLH; 1.
 DR PROSITE; PS50888; HLH; 1.
 KW Acetylation; Developmental protein; DNA-binding;
 KW Myogenesis; Nuclear protein; Transcription regulation.
 FT Myogenesin; Nuclear protein; Basic motif.
 FT DOMAIN; 109 121 Helix-loop-helix motif.
 FT CONFLICT; 122 151 K -> E (In Ref. 2).
 SQ SEQUENCE 319 AA; 34490 MW; AAB935C154318770 CRC64;

Query Match 100.0%; Score 87; DB 1; Length 319;
 Best Local Similarity 100.0%; Pred. No. 1; e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 YSGPPSGARRNCYE 15
Db	212 YSGPPSGARRNCYE 226